Institut Microbiologie, Bioénergies et Biotechnologie
Aix*Marseille Université

PhD position in Microbiology / Biochemistry

(*Laboratoire de Chimie Bactérienne and Laboratoire Architecture et fonction des macromolécules biologiques – CNRS Marseille, France*)

Polysaccharides utilization by Gram-positive bacteria: from genome mining to biochemical characterization

Keywords

Gram-positive bacteria, polysaccharide utilization loci, carbohydrate-active enzymes, ABC-transporter, biomass conversion

Summary of the project

Microbial communities ensure **plant and algal biomass conversion** which is essential for carbon and life cycle. They have **important impact on host health** in mammalian guts with **numerous biotechnological applications**, for example for the valorization of biomass into valuable bioproducts, for health with the design of probiotics, and more generally for sustainable industrial process.

Polysaccharide degradation requires a variety of carbohydrate active enzymes (CAZymes) which are classified in the worldwide reference CAZy database, essential to predict their function (supervisor 2) [1]. To degrade polysaccharides, **Gram-negative Bacteroidetes developed selfish strategies**, sequestrating oligosaccharides and internally depolymerizing them, away from competition. This **strategy relies on polysaccharide utilization loci (PUL)** which are genomic organizations gathering all genes necessary for glycan sensing, transport, depolymerization and the regulation of this process. An algorithm to predict PUL was developed for these bacteria (supervisor 2) [2]. Recently, PUL variant called gpPULs was discovered in Gram-positive bacteria like in the model *Ruminiclostridium cellulolyticum*. In this bacterium, several large gpPULS specific for cellulose, xyloglucan and arabinoxylan utilization were characterized, allowing the import and intracellular degradation of large oligosaccharides composed of up to 9 monosaccharides (supervisor 1) [3,4,5].

Given that only few gpPULs have been characterized in literature to date, **we propose to mine the genomes of Firmicutes to increase the knowledge on polysaccharides utilization by Gram-positive bacteria.** The project aims to **discover new gpPULs** that target new carbohydrates or host new enzymes and transporters, and **to characterize them**. To do so we will use a combination of approaches: (1) **the selection of genomes and gpPUL** based on CAZymes profiles and potential applications; (2) **proteomic and transcriptomic analyses** to validate computational predictions; (3) **biochemical analyses** to characterize the specificity of transporters and the activity of the associated CAZymes. This project relies on the **complementary expertise** of the two co-supervisors, and combines approaches based on **computational prediction associated with biochemical and microbiology studies**.

[1] Drula, E. Garron, M. L. Dogan, S. Lombard, V. Henrissat, B. Terrapon, N. The carbohydrate-active enzyme database: functions and literature. *Nucleic Acids Research*., 2022, PMID: **34850161 – [2]** Terrapon N, Lombard V, Gilbert HJ, Henrissat B. Automatic prediction of polysaccharide utilization lici un Bacteroides species. *Bioinformatics*., 2015, PMID: 25355788 – **[3]** Fosses, A. Maté, M. Franche, N. Liu, N. Denis, Y. Borne, R. de Philip, P. Fierobe, H. P. Perret, S. A seven-gene cluster in *Ruminiclostridium cellulolyticum* is essential for signalization, uptake and catabolism of the degradation products of cellulose hydrolysis. *Biotechnology for Biofuels*., 2017, PMID: 29093754 – **[4]** Ravachol, J. de Philip, P. Borne, R. Mansuelle, P. Maté, M. J. Perret, S. Fierobe, H. P., Mechanisms involved in xyloglucan catabolism by the cellulosome-producing bacterium *Ruminiclostridium cellulolyticum*. *Scientific reports*., 2016, PMID: 26946939 – **[5]** Liu, N., Gagnot, S., Denis Y., Byrne D., Faulds C., Fierobe HP., Perret S. Selfish uptake versus extracellular arabinoxylan degradation in the primary degrader *Ruminiclostridium cellulolyticum*, a new string to its bow. *Biotechnology for Biofuels and bioproducts*, 2022, PMID: 36403068

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The co-supervisors

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Doctoral school

Life and Health Sciences (ED 62), Aix-Marseille université (https://ecole-doctorale-62.univ-amu.fr/)

Expected profile of the candidate

The candidate must hold a Master2 degree by summer 2023 in microbiology or biochemistry and be interested in computational approaches applied to biological sequences.
Good background in molecular biology (PCR, cloning), biochemistry of proteins (purification, SDS-PAGE...), microbiology would be highly appreciated.
Knowledge or interest in bioinformatics (protein sequence analysis), data analysis, or script programming would be appreciated.
Communication skills in French and/or English
Personal skills: Rigorous, curious, well-organized, open-minded

How to apply?

Send us a CV (specifying the English level), a cover letter, transcripts and ranking of Master degree (Master 1 and first semester of Master 2), and the contact information for at least two references by **April 30th 2023.**

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The candidate will be selected by the co-supervisors before May 15th, and the selected candidate will be interviewed on June 6th 2023 by the Institute of Microbiology, Bioenergies and Biotechnology (IM2B) jury which is financing **2 PhD positions among 4 candidates** (starting in October 2023). The modalities of the interview will be given later.